

Table S7  
Power when there are two factors (Normal, 40 genes in a set), for design D2-5

5 samples per group

logFC				100%					25%				
Factor1 (major)	F2	Cor	Cutoff P value	mean	msq	mean50	floormean	GSEAlm	mean	msq	mean50	floormean	GSEAlm
0.06	0.01	0	0.002	0.4	0.17	0.21	0.27	0.63	0.1	0.14	0.12	0.12	0.2
			0.005	0.64	0.24	0.33	0.5	0.63	0.16	0.3	0.26	0.15	0.2
			0.01	0.7	0.37	0.5	0.57	0.74	0.25	0.36	0.37	0.3	0.32
			0.03	0.85	0.66	0.81	0.84	0.84	0.48	0.6	0.59	0.53	0.45
			0.05	0.89	0.73	0.83	0.87	0.91	0.52	0.73	0.69	0.66	0.63
0.06	0.06	0	0.002	0.43	0.23	0.28	0.34	0.73	0.31	0.51	0.51	0.43	0.42
			0.005	0.66	0.31	0.46	0.57	0.73	0.42	0.68	0.64	0.63	0.42
			0.01	0.79	0.5	0.6	0.69	0.82	0.58	0.77	0.75	0.71	0.57
			0.03	0.91	0.7	0.77	0.82	0.86	0.73	0.87	0.82	0.82	0.74
			0.05	0.93	0.73	0.85	0.9	0.91	0.78	0.93	0.91	0.89	0.85
0.15	0.03	0.1	0.002	0.61	0.62	0.55	0.63	0.79	0.08	0.23	0.19	0.17	0.24
			0.005	0.76	0.72	0.76	0.77	0.79	0.15	0.3	0.3	0.27	0.24
			0.01	0.84	0.85	0.85	0.85	0.9	0.24	0.41	0.39	0.39	0.32
			0.03	0.96	0.95	0.95	0.96	0.96	0.41	0.57	0.51	0.51	0.41
			0.05	0.98	0.97	0.97	0.98	0.99	0.48	0.62	0.61	0.56	0.51
0.15	0.15	0.1	0.002	0.52	0.58	0.58	0.55	0.69	0.23	0.48	0.4	0.37	0.39
			0.005	0.73	0.74	0.74	0.72	0.69	0.28	0.59	0.51	0.48	0.39
			0.01	0.82	0.84	0.83	0.82	0.84	0.37	0.66	0.6	0.57	0.5
			0.03	0.91	0.91	0.91	0.92	0.9	0.63	0.79	0.79	0.75	0.69
			0.05	0.94	0.94	0.94	0.93	0.96	0.69	0.87	0.83	0.84	0.77

999 rotations were in ROAST. 125 permutations were in GSEAlm. 100 simulations were run.

“%” represents percentage of up regulated genes in the set.

Table S8  
Power when there are two factors (Normal, 40 genes in a set), for design D2-3

3 samples per group

logFC				100%					25%				
Factor1 (major)	F2	Cor	Cutoff P value	mean	msq	mean50	floormean	GSEAlm	mean	msq	mean50	floormean	GSEAlm
0.06	0.01	0	0.002	0.13	0.04	0.06	0.07	0.16	0.16	0.22	0.21	0.18	0.21
			0.005	0.22	0.12	0.15	0.19	0.16	0.2	0.33	0.32	0.28	0.21
			0.01	0.32	0.2	0.26	0.28	0.34	0.26	0.4	0.41	0.39	0.35
			0.03	0.53	0.36	0.44	0.47	0.48	0.44	0.6	0.57	0.61	0.48
			0.05	0.69	0.44	0.5	0.54	0.7	0.56	0.68	0.69	0.68	0.63
0.06	0.06	0	0.002	0.12	0.03	0.03	0.07	0.19	0.23	0.61	0.57	0.5	0.38
			0.005	0.24	0.08	0.1	0.14	0.19	0.45	0.81	0.75	0.68	0.38
			0.01	0.36	0.16	0.19	0.29	0.4	0.65	0.88	0.82	0.78	0.7
			0.03	0.57	0.38	0.42	0.51	0.54	0.78	0.94	0.93	0.92	0.79
			0.05	0.72	0.44	0.53	0.64	0.73	0.84	0.96	0.95	0.94	0.86
0.15	0.03	0.1	0.002	0.38	0.45	0.44	0.45	0.45	0.06	0.13	0.14	0.1	0.12
			0.005	0.56	0.64	0.64	0.65	0.45	0.12	0.17	0.18	0.17	0.12
			0.01	0.78	0.79	0.81	0.83	0.75	0.15	0.26	0.27	0.24	0.27
			0.03	0.92	0.91	0.92	0.93	0.91	0.35	0.4	0.44	0.39	0.4
			0.05	0.95	0.95	0.95	0.96	0.94	0.45	0.58	0.53	0.54	0.58
0.15	0.15	0.1	0.002	0.46	0.44	0.42	0.47	0.44	0.19	0.51	0.44	0.31	0.43
			0.005	0.66	0.68	0.64	0.7	0.44	0.37	0.65	0.61	0.54	0.43
			0.01	0.79	0.84	0.82	0.83	0.79	0.53	0.76	0.67	0.65	0.56
			0.03	0.93	0.94	0.94	0.95	0.94	0.66	0.87	0.84	0.82	0.7
			0.05	0.96	0.96	0.96	0.96	0.98	0.77	0.9	0.91	0.88	0.84

999 rotations were in ROAST. 125 permutations were in GSEAlm. 100 simulations were run.

“%” represents percentage of up regulated genes in the set.